

Assessment of Generation Interval and Inbreeding in a Peruvian Alpaca Population

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ABSTRACT: Nowadays, information about inbreeding and generation intervals in alpacas from pedigree records to monitoring genetic progress of selection programs, or genetic variability for conservation strategies are scarce. To estimate these parameters, data from 12,493 individuals born from 1999 to 2012 in Mallkinis' Farm - MICHELL Group, in Puno, Peru, were analyzed and processed with the program ENDOG 4.8. Generation intervals obtained were 5.94±0.017, 6.32±0.034, and 5.61±0.034 for the whole population, males and females, respectively, being differences between genders statistically significant. Average inbreeding coefficients were 0.165%±0.0155, 0.17±0.025 and 0.16 ±0.020 for the whole population, males and females, respectively. Only (1.097%) alpacas had inbreeding coefficients greater than 0, with a minimum value of 1.56 % and a maximum of 25%. Furthermore, differences in these parameters were found per type and/or color of alpacas. The results show that the inbreeding in this population is present in a smaller extent.

Keywords: Inbreeding; alpaca; pedigree.

Introduction

Alpaca production is found in a larger extent in the Peruvian Highlands and represents the main livelihood for most of the families who live there (Perez-Cabal et al. (2010)). Nevertheless, the current production system used in this region presents many technical management deficiencies which may result in increased levels of inbreeding, offspring with reduced genetic variation, phenotypic performance, and/or congenital defects (Mc Parland et al. (2007)). The generation interval defined as the average age of the parents at the birth of the offspring or the offspring used for reproduction, is important in a breeding program because it is correlated with the annual rate of genetic change (Falconer (2001)). Both parameters are essential for monitoring populations for mating programs and for management of genetic variability and conservation strategies (Falconer and Mackay (2001); FAO (1998)). However, information about these parameters in alpacas obtained from pedigree records, has been not published until now, mainly because birth recording has been implement during the past fifteen years in most of the Peruvian farms, and pedigree records in their majority still lack of appropriated depth and quality.

Therefore the objectives of this study were to estimate the generation interval and the inbreeding coefficients using one of the larger birth records available from a Peruvian alpaca farm, as a first step to implement monitoring programs of genetic improvement and diversity.

Materials and Methods

Pedigree information. This study was carried out with information from the farm Mallkini owned by Michell Group, located in the district of Muñani, in Azángaro, Puno-Perú. Birth records from 1999 until 2012 were used to structure genealogical records. Data edits were applied to eliminate wrong information at population and individual level.

Determination of genetic parameters. Data was processed using the ENDOG 4.8 program (Gutierrez and Goyache (2005)). Individual inbreeding coefficients (F), defined as the probability that an individual has two alleles identical by descent (Wright (1931)), were calculated by means of the algorithm of Meuwissen and Luo (1992) included in the program. Generation intervals were computed for the 4 paths of selection (fathers-sons, fathers-daughters, mothers-sons and mothers-daughters). Both parameters were computed for the whole population, males, females, Suri, Huacaya, colored and white alpacas. Additionally, the individual increase of inbreeding for the 4th and 5th generation were computed as $\Delta F = 1 - \sqrt[t]{1 - F_i}$, where F_i is the individual coefficients of inbreeding and t is the equivalent complete generations (Gutierrez et al. (2008)). Significant statistically differences were determined with SAS program (SAS/STAT™, 1999) when needed. Finally, percentage of known ancestors per ancestral generation (Boichard (2002)) was used to judge pedigree quality and depth.

Results and Discussion

Records of a total of 12,493 alpacas (44.79% males and 55.21% females, 83.43% Huacaya and 16.87% Suri, 88.71% white and 11.29% colored) in six generations were used. As expected, the proportion of known parents and grandparents was lower, especially for grandparents, because record keeping was recently established in the farm (Figure 1).

The average generation intervals for the entire population, males, and females were 5.938±0.017, 6.319±0.034 and 5,606±0.034, respectively. This parameter was statistically higher for male and Suri alpacas than for female and Huacaya alpacas, respectively (p<0.0001) (Table 1). These results may be related to the fact that males reach sexual maturity at least one year average later than females and also are reproduced for longer periods. Suri alpacas are also keep for breeding for longer periods because they are found in lower proportions than Huacayas and they have been recently revalued due to its fiber characteristics. On the other hand, no differences

were found between colored and white alpacas. This result could be due to the lifetime limit of all alpacas on this farm, no exceptions (Table 1).

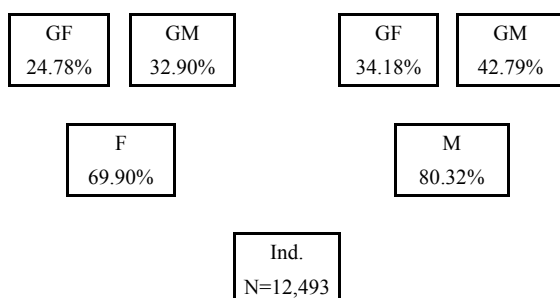


Figure 1: Percentage of known ancestors

[§]GF: Grandfather
^{*}GM: Grandmother
[&]F: Father
[#]M: Mother
[†]Ind: Individuals

Table 1. Generation interval per type and colored of alpacas

		F-S	F-D	M-S	M-D	Total
All alpacas	N	4439	4293	5090	4944	18766
	GI	6.31	6.33	5.62	5.594	5.93
	SE	0.03	0.03	0.03	0.03	0.02
Suri	N	905	897	1017	990	3809
	GI	5.94	6.05	5.65	5.54	5.79
	SE	0.06	0.06	0.08	0.07	0.03
Huacaya	N	3534	3396	4073	3954	14957
	GI	6.40	6.41	5.61	5.601	5.98
	SE	0.04	0.04	0.04	0.04	0.02
White	N	3860	3684	4413	4249	16206
	GI	6.30	6.35	5.63	5.59	5.94
	SE	0.04	0.04	0.04	0.04	0.02
Colored	N	579	609	677	695	2560
	GI	6.36	6.23	5.52	5.61	5.90
	SE	0.09	0.09	0.10	0.10	0.05

[§]N: Number of individuals
[†]GI: Generation Interval
[&]SE: Standard error
[†]F-S: Father-sons
[#]F-D: Father-daughters
[†]M-S: Mother-sons
[‡]M-D: Mother-daughters

The average inbreeding coefficient in the population was $0.165\% \pm 0.0155$, 0.17 ± 0.025 for males and 0.16 ± 0.020 for females. A minimum of 1.56 and a maximum of 25% of inbreeding were found in 1.097% of the individuals; the inbreeding coefficient of the remainders was zero. The highest coefficients were obtained from matings between full siblings, half siblings, and parents and their progeny in 0.04%, 0.53% and 0.30% of the cases, respectively. Also, a higher percentage of inbred individuals was found in Suri or colored alpacas (Table 2), this may be

due to the smaller subpopulations of this individuals that leads to increased crosses between relatives. In general, inbreeding is present in lower levels in the population probably because of the lower pressure of selection compared with other species (Mc Parland et al. (2007); Hamann and Distl (2008)).

Table 2. Number of animals, average inbreeding coefficient (F) and standard error of inbreeding coefficient (SE), for all and only inbred individuals for four alpaca populations.

Popula-tion	All animals			Inbred animals		
	N	F	SE	N	F	SE
Huacaya	10,425	0.14	0.016	9	15.	0.7
				0	76	48
Suri	2068	0.31	0.052	4	14.	1.1
				3	83	01
White	8651	0.08	0.012	6	13.	0.8
				6	42	26
Colored	1410	0.84	0.106	7	16.	0.8
				1	64	75

Related to the evolution of the inbreeding levels in the population, Figure 2 shows an increasing trend since 2008, which can be explained by the increasing pressure of selection due to the implementation of a genetic improvement program and also due increasing pedigree information. Furthermore, average inbreeding rate was estimated only for generations 4 and 5, due to the data depth. Results were $0.295\% \pm 0.0157\%$ and $0.62\% \pm 0.22\%$, respectively. These values were lower than the maximum inbreeding coefficient rate set by FAO (1998) of 1% per generation.

Conclusion

Results indicated that the inbreeding level is low in the population under study; however pedigree deepness is unreliable and should be improved in the future to a better measure of genetic variability. Similar and more complete studies on alpacas' genetic parameters are necessary to implement monitoring programs of diversity and genetic improvement.

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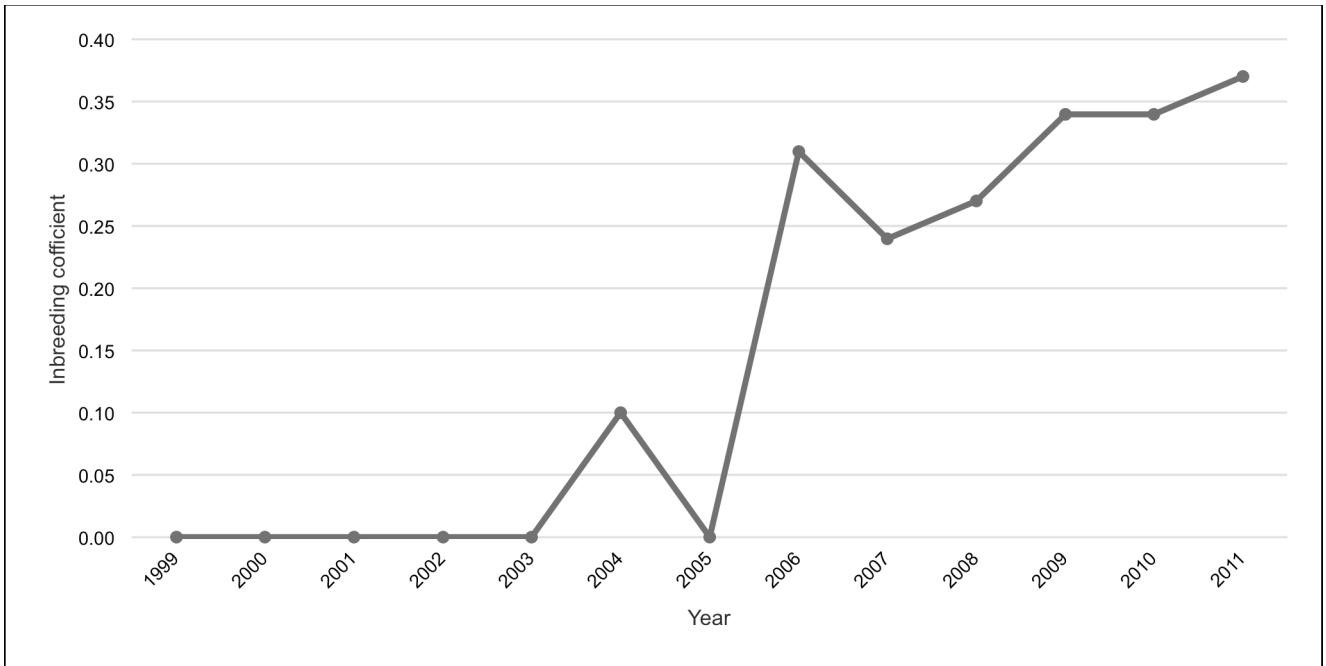


Figure 2: Average inbreeding per year